SEOUENCE LISTING

<110> STONE, EDWIN M. SHEFFIELD, VAL C.

<120> MACULAR DEGENERATION DIAGNOSTICS AND THERAPEUTICS

<130> UIA-018.03

<140> 09/322,357

<141> 1999-05-28

<160> 74

<170> PatentIn Ver. 2.1

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35 40 45

Asp Ile Val Pro Asp Ala Cys Lys Gly Gly Met Lys Cys Val Asn His 50 55 60

Tyr Gly Gly Tyr Leu Cys Leu Pro Lys Thr Ala Gln Ile Ile Val Asn 65 70 75 80

Asn Glu Gln Pro Gln Gln Glu Thr Gln Pro Ala Glu Gly Thr Ser Gly 85 90 95

Ala Thr Thr Gly Val Val Ala Ala Ser Ser Met Ala Thr Ser Gly Val 100 105 110

Leu Pro Gly Gly Gly Phe Val Ala Ser Ala Ala Ala Val Ala Gly Pro 115 120 125

Glu Met Gln Thr Gly Arg Asn Asn Phe Val Ile Arg Arg Asn Pro Ala 130 135 140

Asp Pro Gln Arg Ile Pro Ser Asn Pro Ser His Arg Ile Gln Cys Ala 145 150 155 160

Ala Gly Tyr Glu Gln Ser Glu His Asn Val Cys Gln Asp Ile Asp Glu 165 170 175

Cys Thr Ala Gly Thr His Asn Cys Arg Ala Asp Gln Val Cys Ile Asn 180 185 190

- Leu Arg Gly Ser Phe Ala Cys Gln Cys Pro Pro Gly Tyr Gln Lys Arg 195 200 205
- Gly Glu Gln Cys Val Asp Ile Asp Glu Cys Thr Ile Pro Pro Tyr Cys 210 215 220
- His Gln Arg Cys Val Asn Thr Pro Gly Ser Phe Tyr Cys Gln Cys Ser 225 230 235 240
- Pro Gly Phe Gln Leu Ala Ala Asn Asn Tyr Thr Cys Val Asp Ile Asn 245 250 255
- Glu Cys Asp Ala Ser Asn Gln Cys Ala Gln Gln Cys Tyr Asn Ile Leu 260 265 270
- Gly Ser Phe Ile Cys Gln Cys Asn Gln Gly Tyr Glu Leu Ser Ser Asp 275 280 285
- Arg Leu Asn Cys Glu Asp Ile Asp Glu Cys Arg Thr Ser Ser Tyr Leu 290 295 300
- Cys Gln Tyr Gln Cys Val Asn Glu Pro Gly Lys Phe Ser Cys Met Cys 305 310 315 320
- Pro Gln Gly Tyr Gln Val Val Arg Ser Arg Thr Cys Gln Asp Ile Asn 325 330 335
- Glu Cys Glu Thr Thr Asn Glu Cys Arg Glu Asp Glu Met Cys Trp Asn 340 345 350
- Tyr His Gly Gly Phe Arg Cys Tyr Pro Arg Asn Pro Cys Gln Asp Pro 355 360 365
- Tyr Ile Leu Thr Pro Glu Asn Arg Cys Val Cys Pro Val Ser Asn Ala 370 375 380
- Met Cys Arg Glu Leu Pro Gln Ser Ile Val Tyr Lys Tyr Met Ser Ile 385 390 395 400
- Arg Ser Asp Arg Ser Val Pro Ser Asp Ile Phe Gln Ile Gln Ala Thr 405 410 415
- Thr Ile Tyr Ala Asn Thr Ile Asn Thr Phe Arg Ile Lys Ser Gly Asn 420 425 430 .
- Glu Asn Gly Glu Phe Tyr Leu Arg Gln Thr Ser Pro Val Ser Ala Met 435 440 445
- Leu Val Leu Val Lys Ser Leu Ser Gly Pro Arg Glu His Ile Val Asp 450 455 460
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acacttcatt catgetteat atetaagatt egttgtaaat tgeeceettg ateettteaa 180
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<223> "n" bases at various positions throughout the sequence may
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<223> "n" bases at various positions throughout the sequence may
be a, t, c, g, other or unknown

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aaagaaaaat ccgaatmccg gaaktgttat atttwttaqa aqcattaaat tcctttqqan 420
agattnatca cacatennae taaetgteat teetagaaaa aatatttegg tattteenaa 480
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<210> 64
<211> 312
<212> DNA
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<213> Homo sapiens

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<220>
<223> "n" bases at various positions throughout the sequence may
     be a, t, c, g, other or unknown
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ataattattt taatatagat attttaaatc ttataattta tatatata taatttatat 240
atatatata atccaaagta gtggtgcaca aacttttcaa ctctgtgtcc tttctcttgt 300
                                                                312
ctaattcaac ag
<210> 65
<211> 120
<212> DNA
<213> Homo sapiens
<400> 65
acattgatga atgcagaacc tcaagctacc tgtgtcaata tcaatgtgtc aatgaacctg 60
qqaaattctc atgtatgtgc ccccagggat accaagtggt gagaagtaga acatgtcaag 120
<210> 66
<211> 973
<212> DNA
<213> Homo sapiens
<220>
<223> "n" bases at various positions throughout the sequence may
     be a, t, c, g, other or unknown
<400> 66
qtaaqtttat ttttttttc atatgttagg tatttagttt tagccaggaa gagacaagag 60
gaagttatag gattctccta tagactttca tttttcccac tttcaatata caatttaagc 120
tnttttttcc cctgttcatc ataaaatata tacatctcat aaagagggga ttctatgcta 180
angeogacht ttttegteet taaaagataa ataattttaa taaaatattg atatgtatte 240
tatgtaacct acatcatctn tttgagatac atcttcaaat catccactgg aaaagattca 300
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gggaatanca tncntaaaaa tantttgtaa actataaagc ttgtncaggt caaggggttt 960
ttatnaaatt tac
                                                                973
<210> 67
<211> 766
<212> DNA
<213> Homo sapiens
<400> 67
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tggaacactt catagtttca cttcctgtgc tgtgcttcct ctggacagta taatccactc 120
```

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tgaattcaat acaatgaaca cccagtcttg tgtctaaaag caggttgaac acagtccaga 660
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<211> 124
<212> DNA
<213> Homo sapiens
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agaa
<210> 69
<211> 84
<212> DNA
<213> Homo sapiens
<400> 69
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qaatactttt gtttgtctct gcag
<210> 70
<211> 196
<212> DNA
<213> Homo sapiens
<400> 70
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caaatacatg agcatccgat ctgataggtc tgtgccatca gacatcttcc agatacaggc 120
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agagttctac ctacga
<210> 71
<211> 979
<212> DNA
<213> Homo sapiens
<220>
<223> "n" bases at various positions throughout the sequence may
      be a, t, c, g, other or unknown
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catacccccc aagtaggtat cactaatcat tgatggttaa ttaattatac atagacatac 420
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<210> 72
<211> 418
<212> DNA
<213> Homo sapiens
<220>
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aaggcccca cttcnccann aaaaggaaaa aaaatgntta cmaanagggg gggattcaaa 180
acnaaaaact tttttaaaaa aaaaaaaaag caagtccttg aaacttggag ctaatgactg 240
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<210> 73
<211> 162
<212> DNA
<213> Homo sapiens
<400> 73
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<210> 74
<211> 1111
<212> DNA
<213> Homo sapiens
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